

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 10:47:26 ; Search time 1944 Seconds
(without alignments)
9584.435 Million cell updates/sec

Title: US-09-552-087B-1
Perfect score: 394
Sequence: 1 agctttccctctttgaacaa.....gcgtgactcgcgggatgcgt 394

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		DB	ID	Description
			Match	Length			
c	1	170.2	43.2	86497	8	AP004525	AP004525 Lotus cor
c	2	167	42.4	106033	8	AP006128	AP006128 Lotus cor
c	3	159.4	40.5	4921	8	AF325187	AF325187 Phaseolus

	4	155	39.3	104873	2	AC131249	AC131249	Medicago
	5	152.6	38.7	102538	2	AC144656	AC144656	Medicago
c	6	151	38.3	107317	2	AC147201	AC147201	Medicago
c	7	143	36.3	146274	8	AC149542	AC149542	Populus b
c	8	134.6	34.2	1020	8	AY260959	AY260959	Gossypium
c	9	127	32.2	1001	8	AY260964	AY260964	Gossypium
	10	121.2	30.8	82451	8	AB073160	AB073160	Arabidops
c	11	119.6	30.4	158096	8	AC007887	AC007887	Genomic s
	12	115.6	29.3	143298	8	OSJN00114	AL606994	Oryza sat
c	13	115.6	29.3	174912	2	AC145730	AC145730	Zea mays
	14	114.6	29.1	90627	8	AP000411	AP000411	Arabidops
c	15	114.6	29.1	180651	8	AP005745	AP005745	Oryza sat
	16	114.2	29.0	123080	8	F10A2	AF147259	Arabidops
	17	114.2	29.0	197064	8	ATCHRIV18	AL161506	Arabidops
	18	114	28.9	89281	8	AC006304	AC006304	Arabidops
c	19	114	28.9	138668	8	AC092749	AC092749	Genomic s
c	20	114	28.9	146538	8	AC123594	AC123594	Oryza sat
c	21	114	28.9	300029	8	AE017081	AE017081	Oryza sat
c	22	112.4	28.5	82518	2	AC092077	AC092077	Oryza sat
	23	112.4	28.5	99093	8	OSJN00242	AL731592	Oryza sat
	24	112.4	28.5	113514	8	AP004767	AP004767	Oryza sat
	25	112.4	28.5	117074	2	AP006236	AP006236	Oryza sat
	26	112.4	28.5	120640	8	OSJN00113	AL606991	Oryza sat
	27	112.4	28.5	130433	8	OSJN00066	AL606634	Oryza sat
c	28	112.4	28.5	137020	8	AP005065	AP005065	Oryza sat
c	29	112.4	28.5	139468	8	AC090441	AC090441	Oryza sat
c	30	112.4	28.5	146155	2	AP006445	AP006445	Oryza sat
	31	112.4	28.5	148246	8	AP003054	AP003054	Oryza sat
c	32	112.4	28.5	150485	8	AY360387	AY360387	Oryza sat
c	33	112.4	28.5	153061	2	AP007229	AP007229	Oryza sat
	34	112.4	28.5	158084	8	AP006482	AP006482	Oryza sat
c	35	112.4	28.5	161250	8	AC079634	AC079634	Genomic S
c	36	112.4	28.5	176057	8	AP005067	AP005067	Oryza sat
	37	112.4	28.5	176635	8	AP005832	AP005832	Oryza sat
	38	112.4	28.5	181586	8	OSJN00301	BX890594	Oryza sat
c	39	112.4	28.5	181586	8	OSJN00301	BX890594	Oryza sat
	40	112.4	28.5	184760	8	AP005532	AP005532	Oryza sat
c	41	112.4	28.5	300029	8	AE017080	AE017080	Oryza sat
c	42	112.2	28.5	704	8	AF169186	AF169186	Triticum
c	43	112	28.4	139050	8	AC090054	AC090054	Oryza sat
c	44	112	28.4	142890	8	AP006727	AP006727	Oryza sat
c	45	112	28.4	143959	2	AC090055	AC090055	Oryza sat

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 09:34:50 ; Search time 416 Seconds
(without alignments)
4971.807 Million cell updates/sec

Title: US-09-552-087B-1
Perfect score: 394
Sequence: 1 agctttccctctttgaacaa.....gcgtgactcgcgggatgcgt 394

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	159.4	40.5	4298	6	ABK87139		ABK87139	Scarlet r
c	2	159.4	40.5	4921	6	ABK87140		ABK87140	Scarlet r
c	3	109.2	27.7	1823	10	ADB78908		ADB78908	Rice tran
c	4	106.8	27.1	86584	3	AAF22292		AAF22292	BAC conta
	5	62.2	15.8	163319	3	AAF22306		AAF22306	Arabidops
c	6	54.2	13.8	258	2	AAQ49563		AAQ49563	Beet Cyst
	7	47.8	12.1	963	3	AAC66751		AAC66751	DNA marke

	8	44	11.2	10482	3	AAZ35275	Aaz35275 Soybean r
	9	42	10.7	101786	3	AAF22293	Aaf22293 BAC conta
	10	41.4	10.5	31491	4	AAD10203	Aad10203 Pepper Bs
	11	41.4	10.5	31491	4	AAF63301	Aaf63301 Pepper Bs
	12	41.4	10.5	31491	6	AAK98863	Aak98863 Nucleic a
C	13	40.4	10.3	12286	3	AAZ35261	Aaz35261 Plant gen
	14	40.4	10.3	90336	3	AAF22289	Aaf22289 BAC conta
	15	40.4	10.3	121001	3	AAF22284	Aaf22284 BAC conta
C	16	39.6	10.1	7314	10	ADD25212	Add25212 Fertility
C	17	39.6	10.1	7314	12	ADN61227	Adn61227 Radish nu
	18	39.6	10.1	271990	10	ADD25213	Add25213 Fertility
	19	39.6	10.1	271990	12	ADN61228	Adn61228 Radish nu
C	20	39.4	10.0	4609	3	AAZ35273	Aaz35273 Soybean r
C	21	39.2	9.9	19531	4	ABL10288	Abl10288 Drosophil
	22	37.8	9.6	2000	12	ADJ40989	Adj40989 Plant CDN
	23	37.8	9.6	103929	3	AAF22287	Aaf22287 BAC conta
	24	37.8	9.6	110000	3	AAF22303_2	Continuation (3 of
	25	36.8	9.3	2324	4	ABL28124	Abl28124 Drosophil
C	26	36.8	9.3	5933	6	ABK39977	Abk39977 Human che
C	27	36.8	9.3	10151	6	ABL34433	Abl34433 Human imm
C	28	36.6	9.3	4275	5	ABA19408	Aba19408 Human ner
	29	36.4	9.2	109973	3	AAF22298	Aaf22298 BAC conta
	30	36	9.1	376	3	AAH30289	Aah30289 Human col
C	31	35.8	9.1	6686	6	ABL32461	Abl32461 Human imm
C	32	35.6	9.0	846	10	ADH82676	Adh82676 Enterococ
C	33	35.6	9.0	1782	8	ACA32934	Aca32934 Prokaryot
C	34	35.6	9.0	5259	2	AAX12952	Aax12952 Enterococ
C	35	35.6	9.0	5259	6	ABS98747	Abs98747 Enterococ
	36	35.2	8.9	5216	6	ABL32347	Abl32347 Human imm
	37	35.2	8.9	5216	6	ABL34459	Abl34459 Human met
C	38	35.2	8.9	5884	6	ABK39958	Abk39958 Human che
C	39	35.2	8.9	5884	6	ABL32556	Abl32556 Human imm
	40	34.8	8.8	489	8	ABZ72959	Abz72959 Rice leaf
	41	34.8	8.8	554	4	AAK92583	Aak92583 Human cDN
	42	34.8	8.8	554	12	ADL29010	Adl29010 3' end of
C	43	34.8	8.8	2231	4	AAK94226	Aak94226 Human ful
C	44	34.8	8.8	2231	12	ADL30777	Adl30777 Full leng
C	45	34.8	8.8	2731	2	AAZ00683	Aaz00683 Human GPC

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 11:43:56 ; Search time 85 Seconds
(without alignments)
3294.716 Million cell updates/sec

Title: US-09-552-087B-1
Perfect score: 394
Sequence: 1 agctttccctctttgaacaa.....gcgtgactcgcggggatgcgt 394

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	44	11.2	10482	3	US-09-322-478-23	Sequence 23, Appl
	2	44	11.2	10482	4	US-09-586-106D-23	Sequence 23, Appl
	3	41.4	10.5	31491	3	US-09-360-186-1	Sequence 1, Appli
	4	41.4	10.5	31491	4	US-09-864-680A-1	Sequence 1, Appli
c	5	40.4	10.3	12286	3	US-09-322-478-17	Sequence 17, Appl
c	6	40.4	10.3	12286	4	US-09-586-106D-17	Sequence 17, Appl
c	7	39.4	10.0	4609	3	US-09-322-478-21	Sequence 21, Appl
c	8	39.4	10.0	4609	4	US-09-586-106D-21	Sequence 21, Appl
c	9	35.6	9.0	846	4	US-09-134-000C-561	Sequence 561, App
c	10	35	8.9	916	4	US-09-270-767-10533	Sequence 10533, A
c	11	34.8	8.8	9829	3	US-09-322-478-19	Sequence 19, Appl
c	12	34.8	8.8	9829	4	US-09-586-106D-19	Sequence 19, Appl
c	13	34.6	8.8	12571	3	US-09-322-478-20	Sequence 20, Appl
c	14	34.6	8.8	12571	4	US-09-586-106D-20	Sequence 20, Appl
	15	33.8	8.6	322	4	US-09-513-999C-9792	Sequence 9792, Ap
c	16	32.6	8.3	2801	3	US-08-747-221B-30	Sequence 30, Appl

	17	32.6	8.3	2801	3	US-08-747-221B-32	Sequence 32, Appl
c	18	32.6	8.3	2801	3	US-09-005-051-30	Sequence 30, Appl
	19	32.6	8.3	2801	3	US-09-005-051-32	Sequence 32, Appl
c	20	32.6	8.3	2801	4	US-09-403-942F-30	Sequence 30, Appl
	21	32.6	8.3	2801	4	US-09-403-942F-32	Sequence 32, Appl
c	22	32.6	8.3	2836	3	US-08-747-221B-24	Sequence 24, Appl
	23	32.6	8.3	2836	3	US-08-747-221B-26	Sequence 26, Appl
c	24	32.6	8.3	2836	3	US-09-005-051-24	Sequence 24, Appl
	25	32.6	8.3	2836	3	US-09-005-051-26	Sequence 26, Appl.
c	26	32.6	8.3	2836	4	US-09-403-942F-24	Sequence 24, Appl
	27	32.6	8.3	2836	4	US-09-403-942F-26	Sequence 26, Appl
c	28	32.6	8.3	9139	3	US-09-322-478-22	Sequence 22, Appl
c	29	32.6	8.3	9139	4	US-09-586-106D-22	Sequence 22, Appl
	30	32.4	8.2	861	4	US-09-248-796A-6581	Sequence 6581, Ap
c	31	32.4	8.2	1599	4	US-09-248-796A-5375	Sequence 5375, Ap
c	32	32.4	8.2	4161	3	US-08-790-517-1	Sequence 1, Appli
	33	32.4	8.2	4161	3	US-08-790-517-19	Sequence 19, Appl
c	34	32.2	8.2	3001	4	US-09-539-333D-119	Sequence 119, App
c	35	32.2	8.2	3001	4	US-09-539-333D-225	Sequence 225, App
	36	32	8.1	339	4	US-09-248-796A-12588	Sequence 12588, A
c	37	32	8.1	1004	4	US-09-710-279-4406	Sequence 4406, Ap
	38	32	8.1	1452	4	US-09-710-279-3131	Sequence 3131, Ap
c	39	32	8.1	3926	4	US-09-710-279-4300	Sequence 4300, Ap
	40	32	8.1	7454	4	US-08-836-687B-29	Sequence 29, Appl
	41	32	8.1	21234	4	US-09-810-671-3	Sequence 3, Appli
	42	32	8.1	21234	4	US-10-109-854-3	Sequence 3, Appli
	43	32	8.1	21234	4	US-10-339-656-3	Sequence 3, Appli
c	44	31.8	8.1	1278	4	US-09-540-236-1546	Sequence 1546, Ap
	45	31.8	8.1	1525	4	US-09-270-767-12424	Sequence 12424, A

Run on: January 19, 2005, 10:42:46 ; Search time 436 Seconds
 (without alignments)
 5192.385 Million cell updates/sec

Title: US-09-552-087B-1
 Perfect score: 394
 Sequence: 1 agctttccctctttgaacaa.....gcgtgactcgcgggatgcgt 394

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
c	1	159.4	40.5	4298	10	US-09-997-672-1	Sequence 1, Appli
c	2	159.4	40.5	4921	10	US-09-997-672-2	Sequence 2, Appli
c	3	114.6	29.1	4430	17	US-10-437-963-13434	Sequence 13434, A

C	4	114	28.9	4179	17	US-10-437-963-92684	Sequence 92684, A
C	5	112.4	28.5	943	16	US-10-424-599-4128	Sequence 4128, Ap
C	6	112.4	28.5	3948	17	US-10-437-963-92689	Sequence 92689, A
	7	112.4	28.5	9526	17	US-10-437-963-7171	Sequence 7171, Ap
C	8	112.2	28.5	4179	17	US-10-437-963-92681	Sequence 92681, A
C	9	112	28.4	4354	17	US-10-437-963-49722	Sequence 49722, A
C	10	112	28.4	5252	18	US-10-425-115-134877	Sequence 134877,
C	11	111.4	28.3	425	16	US-10-424-599-73655	Sequence 73655, A
C	12	110.8	28.1	3567	17	US-10-437-963-92685	Sequence 92685, A
C	13	110.8	28.1	6339	17	US-10-437-963-62615	Sequence 62615, A
C	14	109.6	27.8	4185	17	US-10-437-963-21699	Sequence 21699, A
C	15	109.2	27.7	2253	17	US-10-437-963-21708	Sequence 21708, A
C	16	109.2	27.7	2385	17	US-10-437-963-21700	Sequence 21700, A
C	17	109.2	27.7	2443	17	US-10-437-963-13437	Sequence 13437, A
C	18	109.2	27.7	3705	17	US-10-437-963-21697	Sequence 21697, A
C	19	109.2	27.7	3987	17	US-10-437-963-66071	Sequence 66071, A
C	20	109.2	27.7	4704	17	US-10-437-963-21704	Sequence 21704, A
C	21	109.2	27.7	4888	17	US-10-437-963-40278	Sequence 40278, A
C	22	109.2	27.7	5800	17	US-10-437-963-21706	Sequence 21706, A
C	23	109.2	27.7	8937	17	US-10-437-963-40275	Sequence 40275, A
C	24	107.6	27.3	1953	17	US-10-437-963-21710	Sequence 21710, A
C	25	107.6	27.3	5173	17	US-10-437-963-75479	Sequence 75479, A
C	26	107.6	27.3	5388	17	US-10-437-963-40273	Sequence 40273, A
C	27	106	26.9	3263	17	US-10-437-963-80171	Sequence 80171, A
C	28	106	26.9	3493	17	US-10-437-963-75436	Sequence 75436, A
C	29	106	26.9	5004	17	US-10-437-963-40272	Sequence 40272, A
C	30	104.4	26.5	3573	18	US-10-425-115-154154	Sequence 154154,
C	31	104.4	26.5	4322	17	US-10-437-963-75478	Sequence 75478, A
C	32	104.4	26.5	5916	17	US-10-437-963-10457	Sequence 10457, A
C	33	102.2	25.9	7548	17	US-10-437-963-27706	Sequence 27706, A
C	34	101.6	25.8	3045	17	US-10-437-963-16371	Sequence 16371, A
C	35	99.6	25.3	3465	17	US-10-437-963-23576	Sequence 23576, A
C	36	95	24.1	683	16	US-10-424-599-138956	Sequence 138956,
C	37	93.6	23.8	450	16	US-10-424-599-49614	Sequence 49614, A
C	38	91.8	23.3	882	18	US-10-425-115-37826	Sequence 37826, A
C	39	91.6	23.2	459	16	US-10-424-599-84412	Sequence 84412, A
C	40	86.6	22.0	3163	16	US-10-425-114-539	Sequence 539, App
C	41	86.2	21.9	4819	18	US-10-425-115-37820	Sequence 37820, A
	42	85	21.6	3959	18	US-10-425-115-172498	Sequence 172498,
	43	83.4	21.2	2927	18	US-10-425-115-172500	Sequence 172500,
C	44	80.2	20.4	2523	18	US-10-425-115-128079	Sequence 128079,
C	45	76.6	19.4	674	16	US-10-424-599-118164	Sequence 118164,

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 09:06:46 ; Search time 2998 Seconds
(without alignments)
4788.944 Million cell updates/sec

Title: US-09-552-087B-1
Perfect score: 394
Sequence: 1 agctttccctctttgaacaa.....gcgtgactcgcgggatgcgt 394

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
	1	341.4	86.6	879	9	CG824695			CG824695 SOYEW54TV
c	2	339.8	86.2	865	9	CG815847			CG815847 SOYEG76TV
	3	326.8	82.9	410	8	AQ989165			AQ989165 Gm_ISb001
c	4	323.8	82.2	942	9	CG824035			CG824035 SOYDB90TH
	5	322.4	81.8	336	8	AZ254336			AZ254336 Gm_ISb001
c	6	322.2	81.8	699	9	CG816059			CG816059 SOYEG10TH
c	7	315.8	80.2	811	9	CG823173			CG823173 SOYDU73TV
	8	309.4	78.5	878	9	CG813850			CG813850 SOYEV91TH
c	9	308.2	78.2	677	9	CG818759			CG818759 SOYEC73TV

	10	305.4	77.5	900	9	CG819441	CG819441	SOYBB87TV
	11	299.8	76.1	853	9	CG815739	CG815739	SOYAK63TH
C	12	297.2	75.4	714	9	CG821565	CG821565	SOYED15TV
C	13	297	75.4	923	9	CG818159	CG818159	SOYFD28TH
C	14	295.4	75.0	393	8	BH001188	BH001188	Gm_ISb001
	15	263.2	66.8	725	9	CG816698	CG816698	SOYFF16TV
	16	259.8	65.9	799	9	CG819950	CG819950	SOYAU61TV
	17	256.6	65.1	875	9	CG813936	CG813936	SOYCC76TH
C	18	226.2	57.4	609	8	BH001177	BH001177	Gm_ISb001
	19	218.4	55.4	826	9	CG818259	CG818259	SOYDL07TV
C	20	195.4	49.6	562	8	BH001345	BH001345	Gm_ISb001
	21	179.4	45.5	363	9	CG824057	CG824057	SOYBA93TH
C	22	158.8	40.3	901	9	CG825863	CG825863	SOYDB92TH
	23	154.8	39.3	686	9	CG824150	CG824150	SOYAD65TV
C	24	152.6	38.7	786	9	CG937169	CG937169	MBEEK50TR
C	25	151.8	38.5	829	9	CG928329	CG928329	MBEGV02TF
	26	151	38.3	918	9	CG817392	CG817392	SOYEN64TH
C	27	150.2	38.1	708	9	CG824748	CG824748	SOYEH10TH
	28	143.6	36.4	790	9	CG825632	CG825632	SOYAH52TH
	29	143.6	36.4	944	9	CG823977	CG823977	SOYEV75TH
	30	140.4	35.6	752	9	CG822945	CG822945	SOYAH76TH
	31	139.2	35.3	741	9	CC967985	CC967985	BOIBX71TF
	32	137.6	34.9	718	8	BH439807	BH439807	BOGFN48TR
C	33	136	34.5	691	8	BH944399	BH944399	obu89e04.
	34	136	34.5	740	8	BH537723	BH537723	BOGNP83TR
C	35	135.6	34.4	649	8	BH588561	BH588561	BOGHY13TF
	36	135.4	34.4	218	9	CG812963	CG812963	SOYAH86TH
	37	134.4	34.1	675	8	BH967822	BH967822	odh56g11.
C	38	134.4	34.1	702	8	BZ509650	BZ509650	BOMRR92TR
	39	134.4	34.1	754	8	BH483356	BH483356	BOHAG59TR
C	40	134.4	34.1	801	8	BZ502790	BZ502790	BONPJ38TF
	41	134.4	34.1	883	8	BH560883	BH560883	BOGKP80TR
C	42	133.4	33.9	693	8	BZ040126	BZ040126	lka21c07.
	43	132.4	33.6	528	9	AG226204	AG226204	Lotus cor
C	44	131.4	33.4	647	8	BH572120	BH572120	BOGOF78TR
	45	131.2	33.3	524	8	BH552018	BH552018	BOHKM40TR